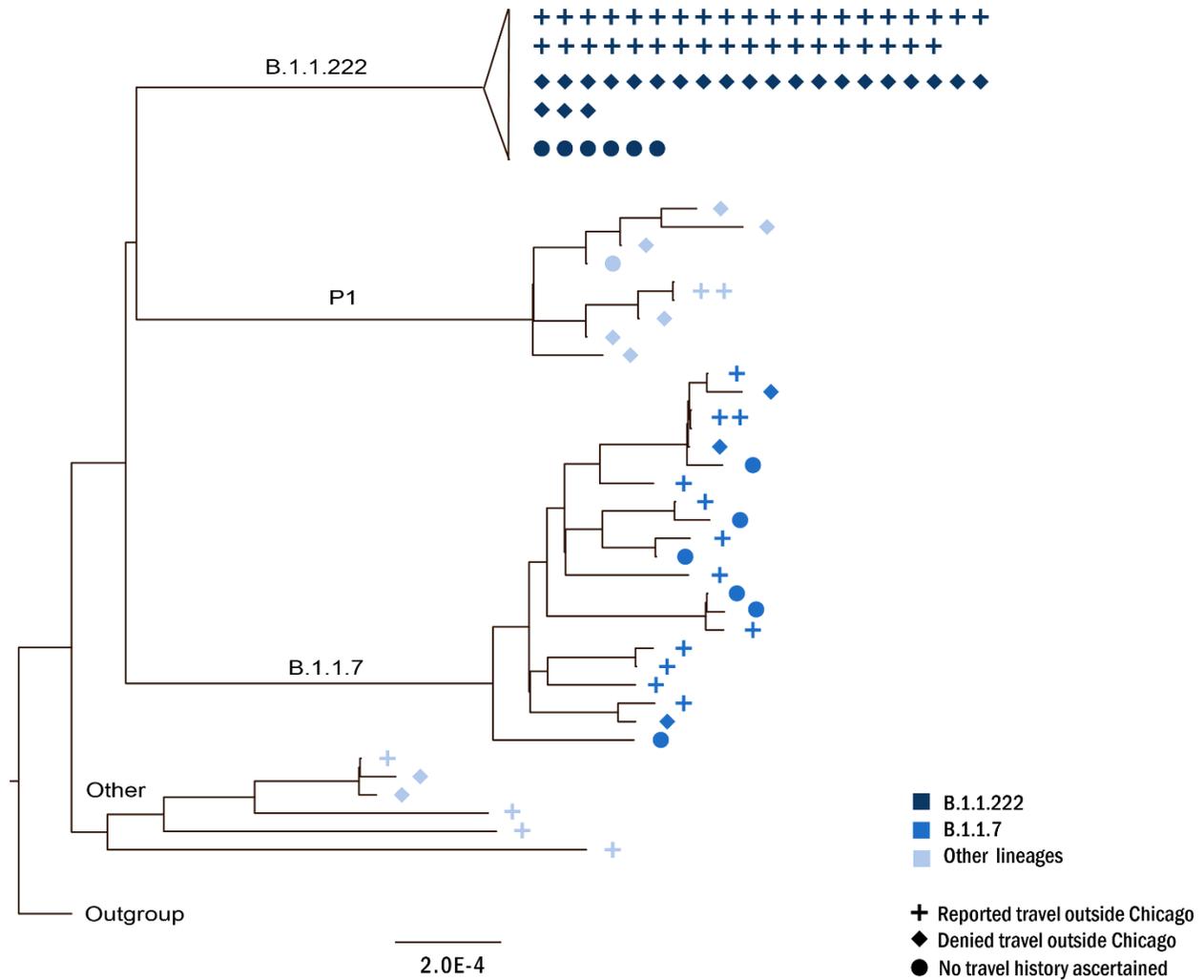


**SUPPLEMENTARY FIGURE. Phylogenetic tree showing genetic distance\* between SARS-CoV-2-positive specimens associated with a university outbreak† by travel history (n = 104) — Chicago, Illinois, March–May 2021**



\* Genetic distance based on substitutions per site is indicated by length of branches. Phylogenetic tree constructed using maximum likelihood estimates. An outgroup (a more distantly related group) is shown for reference (Wuhan isolate EPI\_ISL\_406798 | hCoV-19/Wuhan/WH01/2019 | China | 2019-12-26 | B). B.1.1.222 sequences had no visible mutations and are grouped together. Other lineages include B.1.526, B.1.526.1, B.1.526.2, and B.1.429. Among the specimens of B.1.1.222 lineage, the majority of sequences were genetically similar (within two nucleotides). Although there is no standard genomic definition of sequences linked by transmission, this level of similarity, together with the lack of detection of similar contemporaneous specimens in Chicago, is likely consistent with one viral introduction.

† Specimens from 104 of 158 students with SARS-CoV-2 infection were successfully sequenced.